

Serial Number: 09/895,211

CRF Processing Date: 11/16/91  
 Edited by: DC  
 Verified by: DC (STIC sta

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/lifename at end of file.  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: The fields in Seq. ID 5 were all in one line. Used return key to break out field to get on its own line.  
then

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

OIPE

## RAW SEQUENCE LISTING

DATE: 11/16/2001

PATENT APPLICATION: US/09/895,211

TIME: 11:27:14

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\11162001\I895211.raw

3 <110> APPLICANT: Hunton and Williams  
 4 Emorine, Laurent  
 6 <120> TITLE OF INVENTION: INTRON/EXON STRUCTURE OF THE HUMAN AND MOUSE BETA3  
 ADRENERGIC RECEPTOR

7 GENES

9 &lt;130&gt; FILE REFERENCE: 58769.000011

11 &lt;140&gt; CURRENT APPLICATION NUMBER: 09/895,211

13 &lt;141&gt; CURRENT FILING DATE: 2001-07-02

15 &lt;160&gt; NUMBER OF SEQ ID NOS: 9

17 &lt;170&gt; SOFTWARE: PatentIn version 3.1

W--&gt; 18 &lt;210&gt; SEQ ID NO: 1

19 &lt;211&gt; LENGTH: 3683

20 &lt;212&gt; TYPE: DNA

21 &lt;213&gt; ORGANISM: Homo sapiens

23 &lt;400&gt; SEQUENCE: 1

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28 actccagcgg gttacctttg cctctgatac ataaaggggtg gggatgggag cgctctcttc      180
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42 agtcgctctc atgccttget gtccctcccc ctgagccagg tgatttggga gacccctcc      600
44 ttctttcttt cctaccgcc ccacgcgcga ccgggggatg gctccgtggc ctacagagaa      660
46 cagctctctt gcccatggc cggacctccc caccctggcg cccaatacgg ccaacaccag      720
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52 ccagaccatg accaactgtt tctgacttcc gctggccgca gccgacctgg tgatgggact      900
54 cctggtggtg ccgcggcgcg ccaccttggc gctgactggc cactggccgt tgggcgccac      960
56 tggctgcgag ctgtggacct cgggtggact gctgtgtgtg accgccagca tcgaaacct      1020
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60 ggtcaccaag cgctgcgccc ggacagctgt ggtcctgtgt tgggtcgtgt cggccgcggt      1140
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78 ccttgccctg aactggctag gttatgcaa ttctgccttc aaccgcctca tctactgcg      1680
80 cagcccgac ttgcgcagc ccttcgcggc tcttctgtgc cgctgcggcc gtgcgctgcc      1740
82 tccggagccc tgcgcgcgg ccgcgccggc cctcttcccc tcgggcgttc ctgcggccc      1800
84 gagcagccca gcgcagccca ggctttgcca acggctcgac gggtaggtaa ccggggcaga      1860
86 gggaccggcg gctcagggtc ggaagcatg cgatgtgtcc gtgggtcaac tttttgagt      1920
88 tggagtatat taagagaagg tgggatggct ttgcttgag agaaaaggga acgaggagta      1980

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TIME: 11:27:14

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94 cgctgcggtg tcccaggac tctgcctcg cctggtcggc tttagggatt tttttttttt 2160
96 ttaaataagag acaggggttc gtctctgtcg ccacgcggg aatgcagtggt tgcgatctca 2220
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138 cagtgtcaga aggacttcgc cagggttttg ggagctccag gggtcataag aaggtgaacc 3480
140 attagaacag atcccttctt ttccctttgc aatcagataa ataaatatca ctgaatgcag 3540
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150 &lt;210&gt; SEQ ID NO: 2

151 &lt;211&gt; LENGTH: 408

152 &lt;212&gt; TYPE: PRT

153 &lt;213&gt; ORGANISM: Homo sapiens

155 &lt;400&gt; SEQUENCE: 2

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156 Met Ala Pro Trp Pro His Glu Asn Ser Ser Leu Ala Pro Trp Pro Asp
157 1 5 10 15
160 Leu Pro Thr Leu Ala Pro Asn Thr Ala Asn Thr Ser Gly Leu Pro Gly
161 20 25 30
164 Val Pro Trp Glu Ala Ala Leu Ala Gly Ala Leu Leu Ala Leu Ala Val
165 35 40 45
168 Leu Ala Thr Thr Gly Val Asn Leu Leu Val Ile Val Ala Ile Ala Trp
169 50 55 60
172 Thr Pro Arg Leu Gln Thr Met Thr Asn Val Phe Val Thr Ser Leu Ala
173 65 70 75 80
176 Ala Ala Asp Leu Val Met Gly Leu Leu Val Val Pro Pro Ala Ala Thr
177 85 90 95
180 Leu Ala Leu Thr Gly His Trp Pro Leu Gly Ala Thr Gly Cys Glu Leu
181 100 105 110
184 Trp Thr Ser Val Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu

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PATENT APPLICATION: US/09/895,211

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188 Cys Ala Leu Ala Val Asp Arg Tyr Leu Ala Val Thr Asn Pro Leu Arg
189          130          135          140
192 Tyr Gly Ala Leu Val Thr Lys Arg Cys Ala Arg Thr Ala Val Val Leu
193 145          150          155          160
196 Val Trp Val Val Ser Ala Ala Val Ser Phe Ala Pro Ile Met Ser Gln
197          165          170          175
200 Trp Trp Arg Gly Val Ala Asp Ala Glu Ala Gln Arg Cys His Ser Asn
201          180          185          190
204 Pro Arg Cys Cys Ala Phe Ala Ser Gln Met Pro Tyr Val Leu Leu Ser
205          195          200          205
208 Ser Ser Val Ser Phe Tyr Leu Pro Leu Leu Val Met Leu Phe Val Tyr
209          210          215          220
212 Ala Arg Val Phe Val Val Ala Thr Arg Gln Leu Arg Leu Leu Arg Gly
213 225          230          235          240
216 Glu Leu Gly Arg Phe Pro Pro Glu Glu Ser Pro Pro Ala Pro Ser Arg
217          245          250          255
220 Ser Leu Ala Pro Ala Pro Val Gly Thr Cys Ala Pro Pro Glu Gly Val
221          260          265          270
224 Pro Ala Cys Gly Arg Arg Pro Ala Arg Leu Leu Pro Leu Arg Glu His
225          275          280          285
228 Arg Ala Leu Cys Thr Leu Gly Leu Ile Met Gly Thr Phe Thr Leu Cys
229          290          295          300
232 Trp Leu Pro Phe Phe Leu Ala Asn Val Leu Arg Ala Leu Gly Gly Pro
233 305          310          315          320
236 Ser Leu Val Pro Gly Pro Ala Phe Leu Ala Leu Asn Trp Leu Gly Tyr
237          325          330          335
240 Ala Asn Ser Ala Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe
241          340          345          350
244 Arg Ser Ala Phe Arg Arg Leu Leu Cys Arg Cys Gly Arg Arg Leu Pro
245          355          360          365
248 Pro Glu Pro Cys Ala Ala Ala Arg Pro Ala Leu Phe Pro Ser Gly Val
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257          405
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264 <213> ORGANISM: Mus musculus
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271 agaagagggg ctatcttgga tggtttgggt tgttcggttt tgttttggtt tgtttctgga 180
273 tggttgcctt ccttggtggg taaaggatag ggtgcggggg tttctcttct ttgcagggtt 240
275 gcctcagggt ctgccaggaa ggagctgctg agctccagga aaccgggtgct gagggagtgt 300
277 caagacagga cgccctctc caccctccaa ttcccaccag aggcctctct tgtgactatt 360
279 ggacgctggt cttttaaag cagccactcc tcccggaac taggggtgtac atgggggggtg 420

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285	accttcccac	cccaggcgcc	acacgagatg	gctccgtggc	ctcacagaaa	cggctctctg	600
287	gctttgtggt	cggacgcccc	taccctggac	cccagtgcag	ccaacaccag	tgggttgcca	660
289	ggagtacat	gggcagcggc	attggctggg	gcattgctgg	cgctggccac	ggtgggaggc	720
291	aacctgctgg	taatcatagc	catgcccgcc	acgccgagac	tacagaccat	aaccaacgtg	780
293	ttcgtgactt	cactggccgc	agctgacttg	gtagtgggac	tcctcgtaat	gccaccaggg	840
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303	agccagtggg	ggcgtgtagg	ggcagatgcc	gaggcacagg	aatgccactc	caatccgcgc	1140
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313	tgcggccggc	ggcctgcgcg	cctcctgcc	ctccgggaac	accgcgcctt	gcgcacctta	1440
315	ggtctcatta	tgggcatctt	ctctctgtgc	tggctgccct	tcttcctggc	caacgtgctg	1500
317	cgcgcactcg	cggggccctc	tctagtcccc	agcggagttt	tcctcgcctt	gaactggctg	1560
319	ggctatgcc	actccgcctt	caaccgcgtc	atctactgcc	gcagcccggg	ctttcgcgac	1620
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335	ttggggtttg	tttgtttttg	tttgtttgtt	tgtttgtttt	gttttttttag	ttccctctct	2100
337	cgggaaccca	ggcatctcta	tacctgtctg	ggatatccat	agacagcaat	ggacttccct	2160
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367	gtttgaggtt	tcctccctgt	ctcctcacta	tggctctcta	agcaccatct	tggaccatct	3060
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386 <211> LENGTH: 400
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396 20 25 30
399 Val Pro Trp Ala Ala Ala Leu Ala Gly Ala Leu Leu Ala Leu Ala Thr
400 35 40 45
403 Val Gly Gly Asn Leu Leu Val Ile Ile Ala Ile Ala Arg Thr Pro Arg
404 50 55 60
407 Leu Gln Thr Ile Thr Asn Val Phe Val Thr Ser Leu Ala Ala Ala Asp
408 65 70 75 80
411 Leu Val Val Gly Leu Leu Val Met Pro Pro Gly Ala Thr Leu Ala Leu
412 85 90 95
415 Thr Gly His Trp Pro Leu Gly Glu Thr Gly Cys Glu Leu Trp Thr Ser
416 100 105 110
419 Val Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Ala Leu
420 115 120 125
423 Ala Val Asp Arg Tyr Leu Ala Val Thr Asn Pro Leu Arg Tyr Gly Thr
424 130 135 140
427 Leu Val Thr Lys Arg Arg Ala Arg Ala Ala Val Val Leu Val Trp Ile
428 145 150 155 160
431 Val Ser Ala Ala Val Ser Phe Ala Pro Ile Met Ser Gln Trp Trp Arg
432 165 170 175
435 Val Gly Ala Asp Ala Glu Ala Gln Glu Cys His Ser Asn Pro Arg Cys
436 180 185 190
439 Cys Ser Phe Ala Ser Asn Met Pro Tyr Ala Leu Leu Ser Ser Ser Val
440 195 200 205
443 Ser Phe Tyr Leu Pro Leu Leu Val Met Leu Phe Val Tyr Ala Arg Val
444 210 215 220
447 Phe Val Val Ala Lys Arg Gln Arg His Leu Leu Arg Arg Glu Leu Gly
448 225 230 235 240
451 Arg Phe Ser Pro Glu Ser Pro Pro Ser Pro Ser Arg Ser Pro Ser
452 245 250 255
455 Pro Ala Thr Gly Gly Thr Pro Ala Ala Pro Asp Gly Val Pro Pro Cys
456 260 265 270
459 Gly Arg Arg Pro Ala Arg Leu Leu Pro Leu Arg Glu His Arg Ala Leu
460 275 280 285
463 Arg Thr Leu Gly Leu Ile Met Gly Ile Phe Ser Leu Cys Trp Leu Pro
464 290 295 300
467 Phe Phe Leu Ala Asn Val Leu Arg Ala Leu Ala Gly Pro Ser Leu Val
468 305 310 315 320
471 Pro Ser Gly Val Phe Ile Ala Leu Asn Trp Leu Gly Tyr Ala Asn Ser
472 325 330 335

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/895,211

DATE: 11/16/2001

TIME: 11:27:15

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